Replacement Sheet

```
                VH
                F1                                                  CDR1      F2
10F6      1 MAQVQLQESGGEMKKPGESLKISCKGYGYSFATSWIGWVRQMPGRGLEWM
5E5       1 MAEVQLVQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWV
10D10     1 MAEVQLVQSGGGVVQPGGSLSLSCAVSGITLRTYGMHWVRQAPGKGLEWV
12B5      1 MAQVQLVQSGGGLVRPGGSLSLSCAVSGITLRTYGMHWVRQAPGKGLEWV
12D5      1 MAQVQLVESGGGLVKPGGSLRLSCAASGFTFSSHNMNWVRQAPGKGLEWV
12E10     1 MAQVQLQQSGPGLVKPSETLSLTCTVSGDSISSYYWSWIRQPPGKGLEWI

                CDR2                          F3
10F6     51 AIMYPGNSDTRHNPSFEDQVTMSADTSINTAYLQWSSLKASDTAMYYCAR
5E5      51 SYISSSGSTIYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
10D10    51 AGISFDGRSEYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
12B5     51 AGISFDGRSEYYADSVQGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCAR
12D5     51 SSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
12E10    51 GYIYYSGS-TNYNPSLKSRVTISVDTSKSQFSLKLSSVTAADTAVYYCAR

                CDR3          F4                          VL      F1
10F6    101 AGVAGGAFDLWGKGTMVTVSSGGGGSGGGGSGGGGSQSVLTQ-PASVSGS
5E5     101 -WSGEDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIVMTQSPSTLSAS
10D10   101 -DRGSYGMDVWGRGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSAS
12B5    101 -G-AHYGFDIWGQGTMVTVSSGGGGTGGGGSGGGGSDIQMTQSPSTLSAS
12D5    101 -DRGSTGMDVWGRGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSAS
12E10   100 ----GRYFDVWGRGTMVTVSSGGGGSGGGGSGGGGSSYVLTQ-PPSVSGS

                          CDR1          F2                CDR2
10F6    150 PGQSITISCTGTSSGVGGYNYVSWYQQHPGKAPKLLIYGNSNRPSGVPDR
5E5     150 VGDRVAITCRASE---GIYHWLAWYQQKPGKAPKLLIYKASSLASGAPSR
10D10   150 IGDRVTITCRASE---GIYHWLAWYQQKPGKAPKLLIYKASSLASGAPSR
12B5    149 IGDRVTITCRASE---GIYHWLAWYQQKPGKAPKLLIYKASSLASGAPSR
12D5    150 IGDRVTITCRASE---GIYHWLAWYQQKPGKAPKLLIYKASSLASGAPSR
12E10   145 PGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEGSKRPSGVSNR

                F3                                CDR3      F4
10F6    200 FSASKSGNTASLTISGLQAEDEADYFCSTYAPPGIIMFGGGTKLTVLGAA
5E5     197 FSGSGSGADFTLTISSLQPDDFATYYCQQYSNYPL-TFGGGTKLEVKRAA
10D10   197 FSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPL-TFGGGTKLEILRAA
12B5    196 FSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPL-TFGGGTELEIKRAA
12D5    197 FSGSGSGTDFTXTISSLQPDDFATYYCQQYSNYPL-TFGGGTKLEIKRAA
12E10   195 FSGSKSGNTASLTISGLQAEDEADYYCSSYTTRSTRVFGGGTKLTVLGAA
```

FIG._1

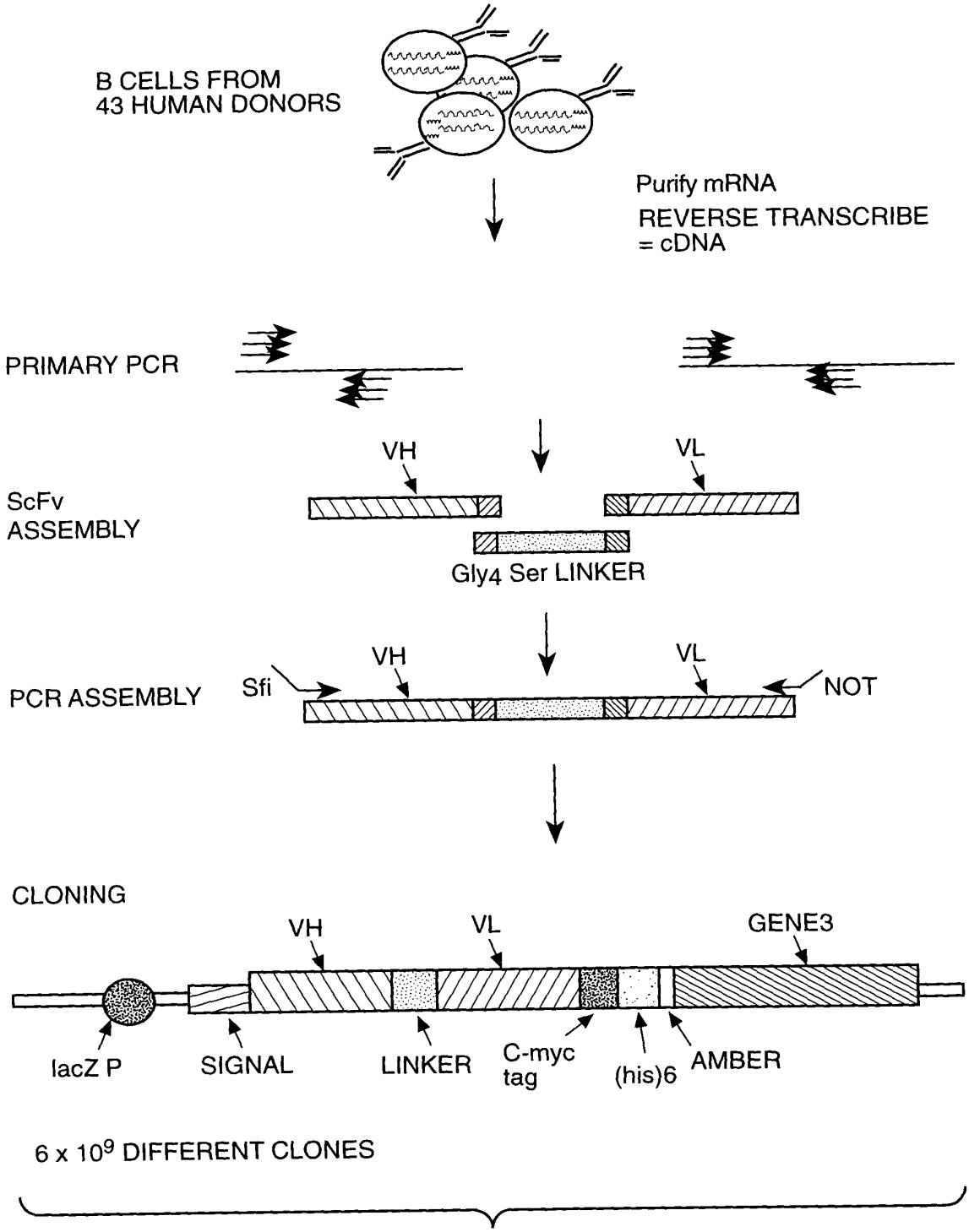
B CELLS FROM
43 HUMAN DONORS
Purify mRNA
REVERSE TRANSCRIBE
= cDNA
PRIMARY PCR
ScFv
ASSEMBLY
VH
VL
Gly4 Ser LINKER
PCR ASSEMBLY
Sfi
NOT
CLONING
GENE3
lacZ P
SIGNAL
LINKER
C-myc
tag
(his)6
AMBER
6 x 10^9 DIFFERENT CLONES

FIG._2

86T280*T6086T60

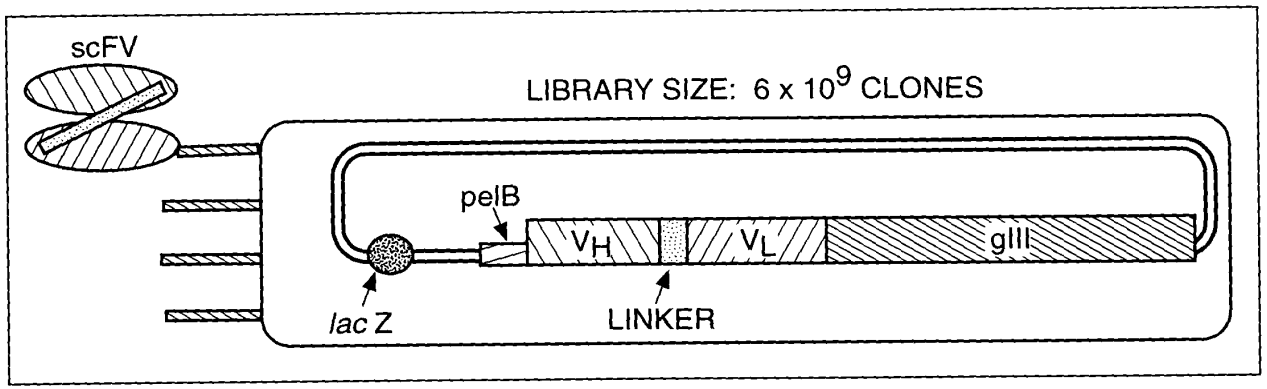

FIG._3

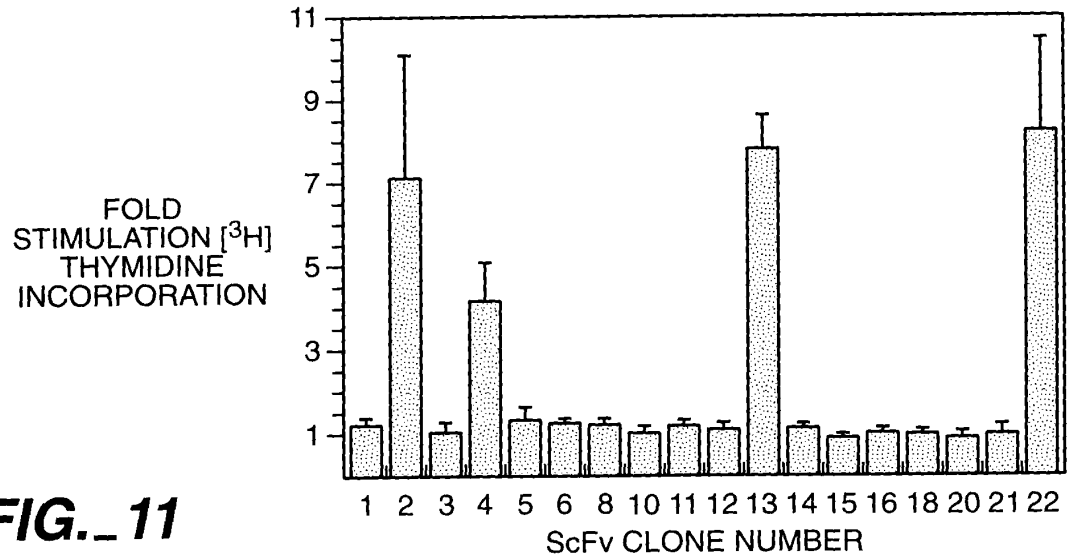

FIG._11

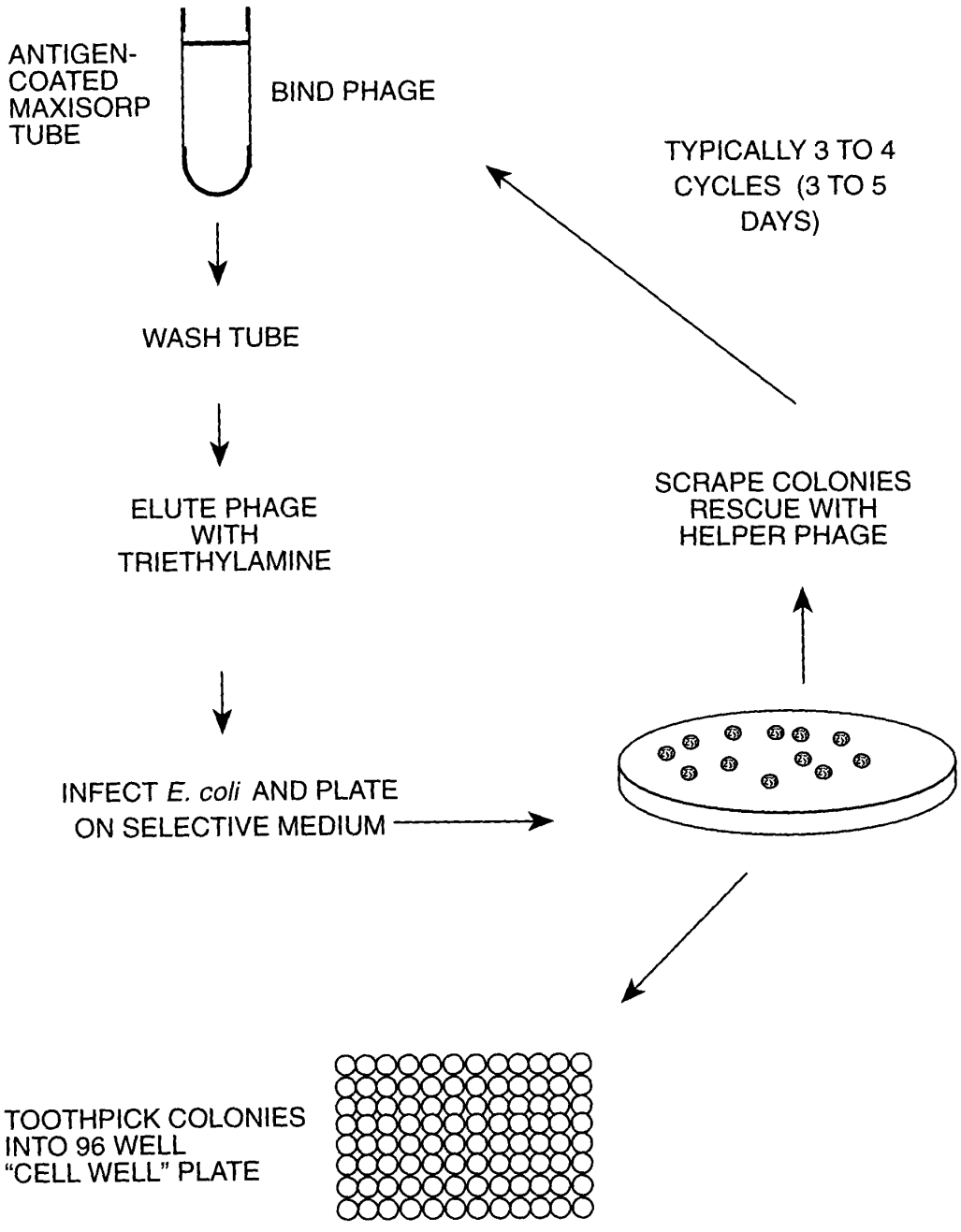

FIG._4

86T250 T6022T50

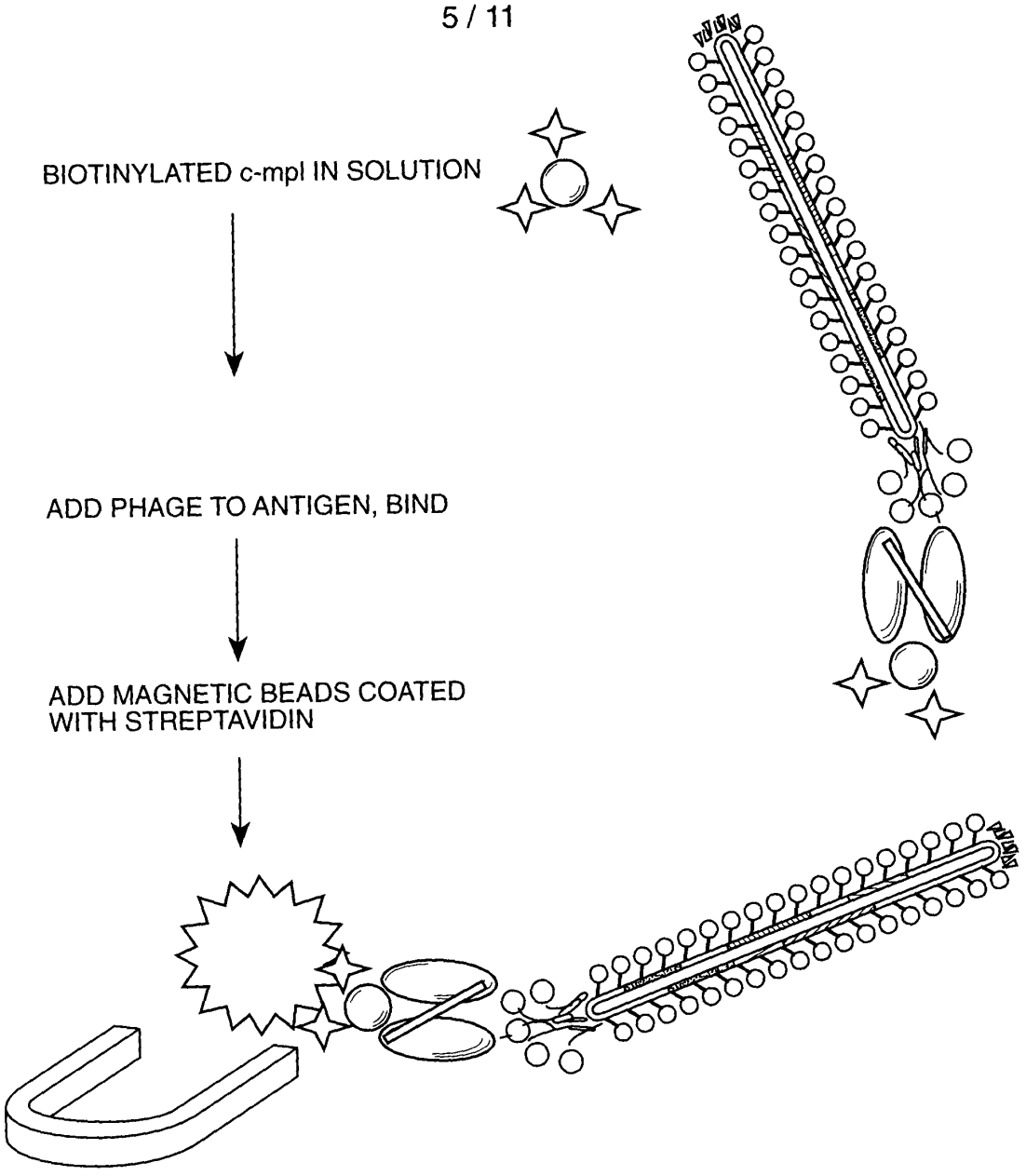
BIOTINYLATED c-mpl IN SOLUTION
ADD PHAGE TO ANTIGEN, BIND
ADD MAGNETIC BEADS COATED WITH STREPTAVIDIN
PULL OUT BOUND PHAGE WITH MAGNET
WASH, ELUTE, INFECT
USE DECREASING ANTIGEN CONCENTRATIONS TO SELECT FOR HIGHEST AFFINITY PHAGE

FIG._5

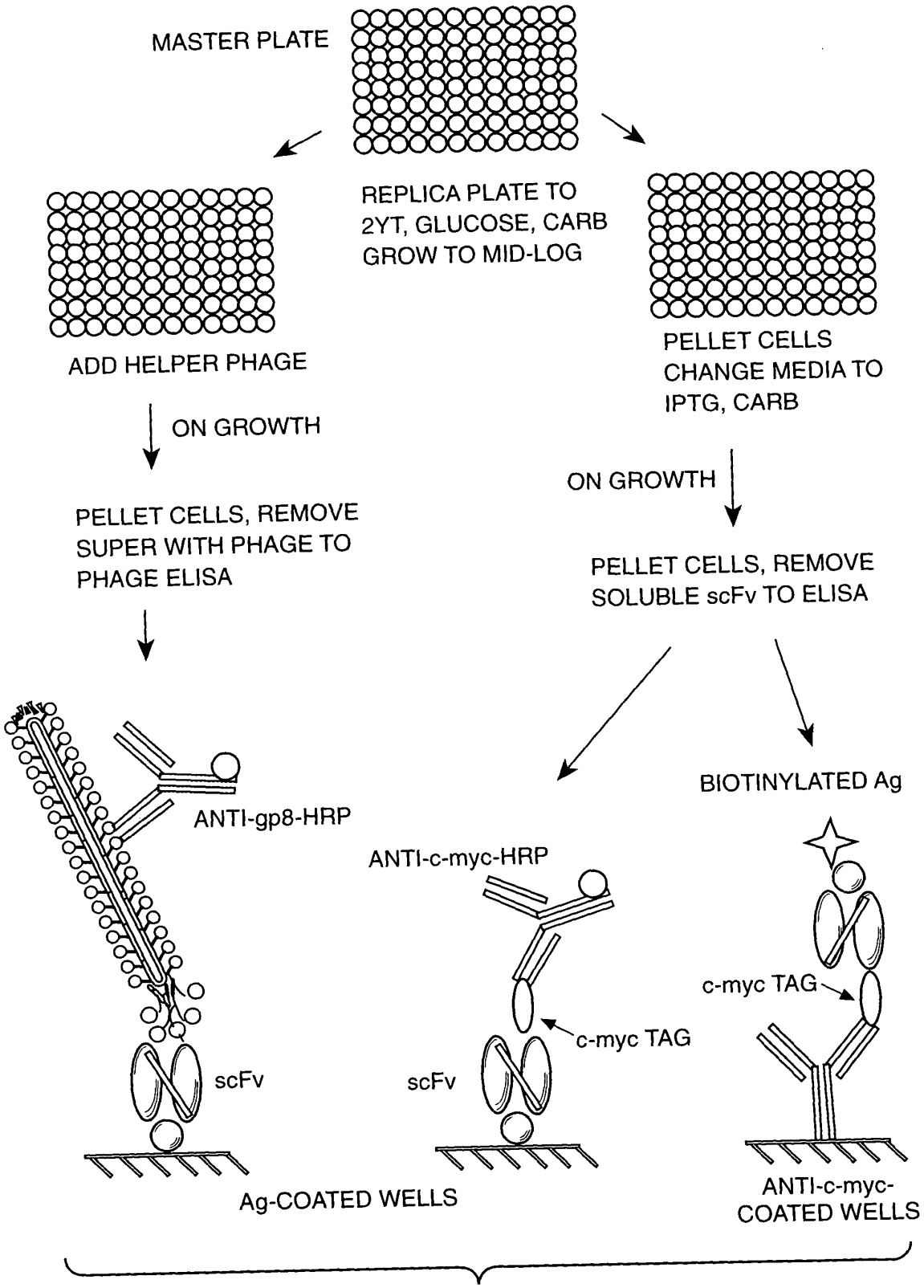

FIG._6

SUBSTITUTE SHEET (RULE 26)

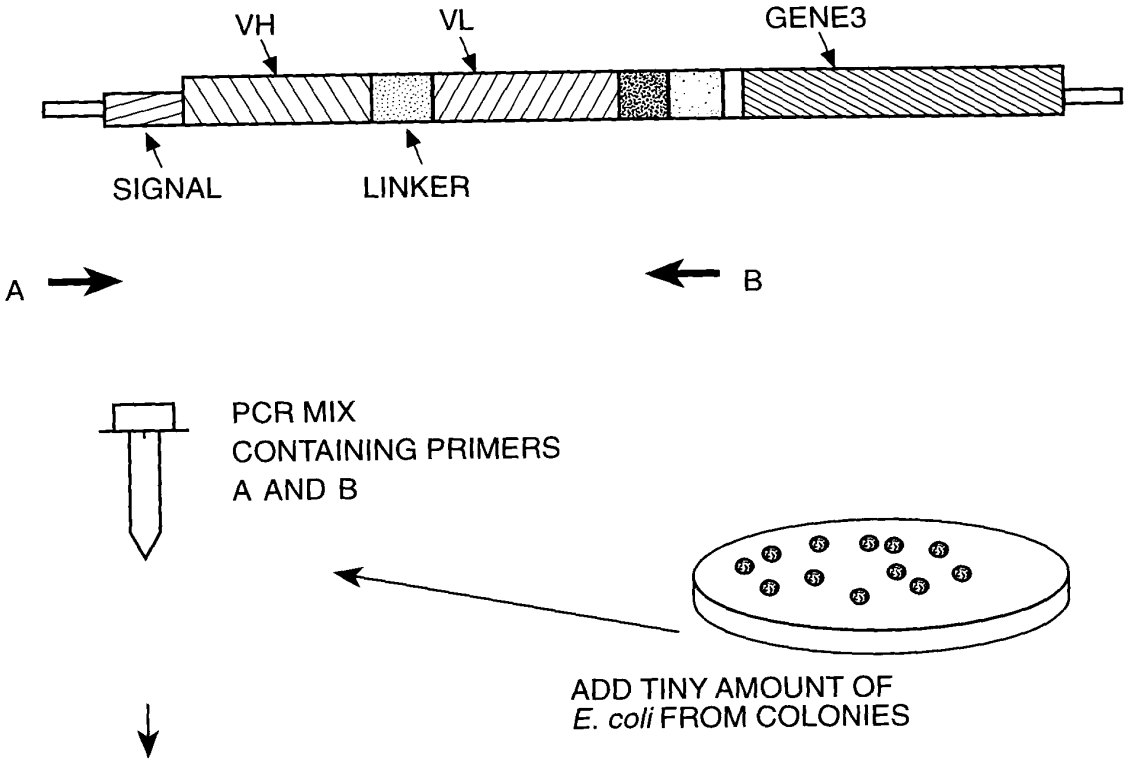
VH
VL
GENE3
SIGNAL
LINKER
A
B
PCR MIX
CONTAINING PRIMERS
A AND B
ADD TINY AMOUNT OF
E. coli FROM COLONIES
1Kb BAND IN SEEN ON AGAROSE GEL
DIGEST WITH RESTRICTION ENZYME BstNI
ANALYZE PRODUCTS ON 3% AGAROSE GEL

FIG._7

jc540 U.S. PTO
09/138091
08/21/98

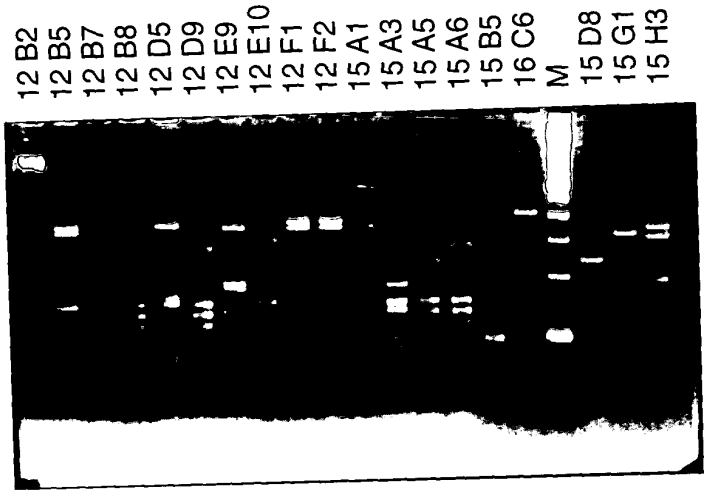

FIG._8A

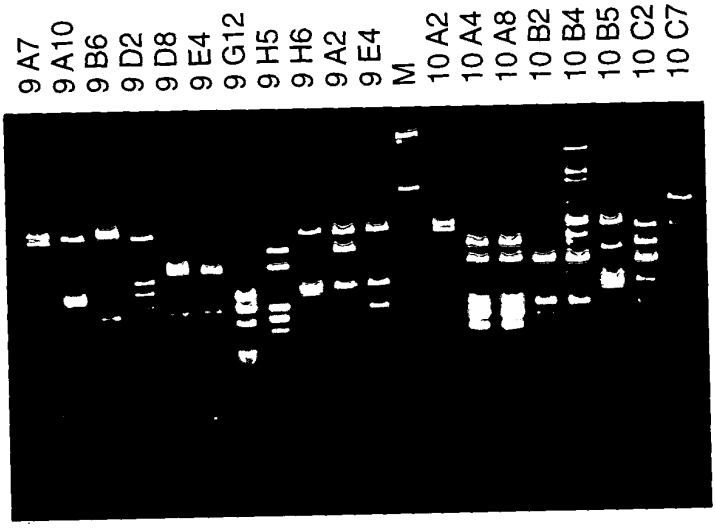

FIG._8B

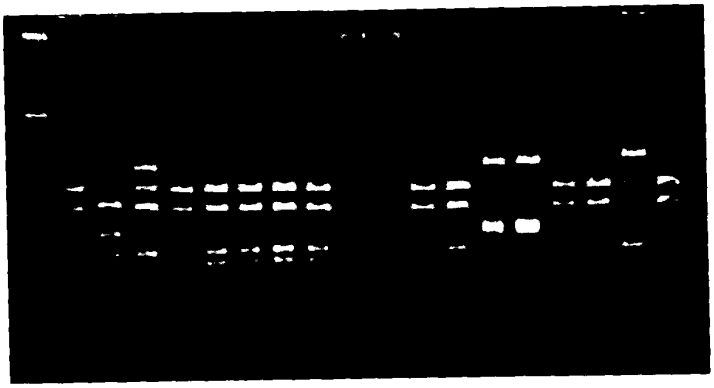

FIG._8C

96T280"T608ET60

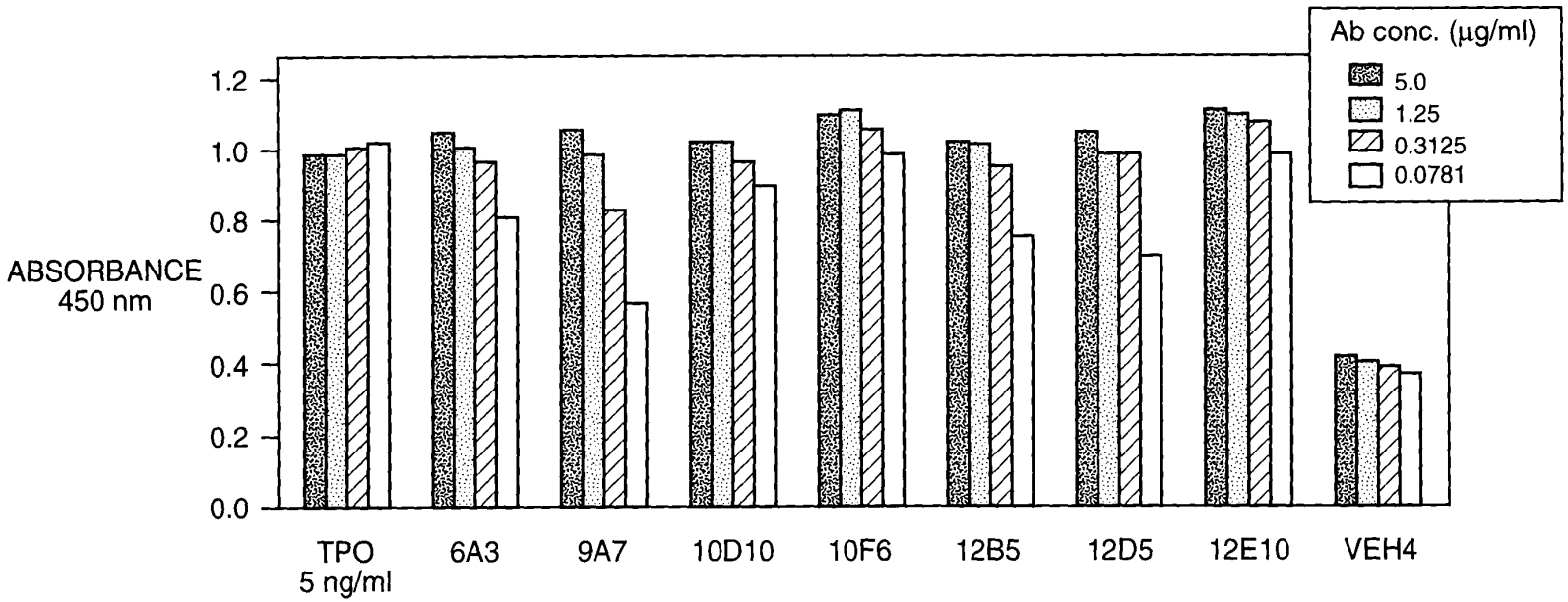

FIG._9

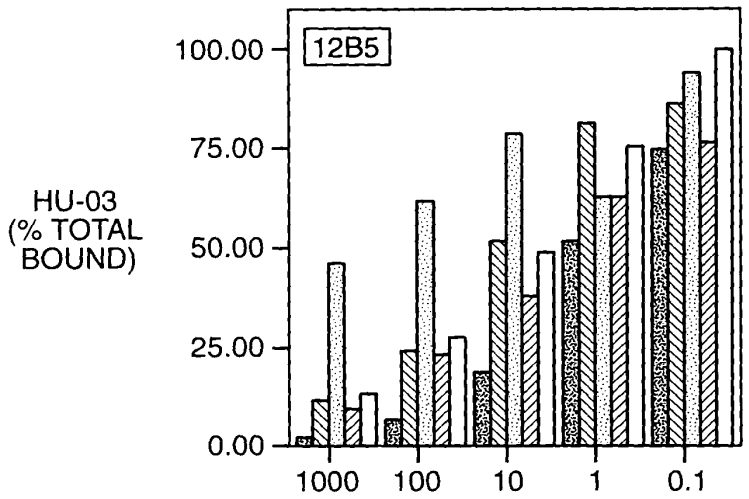

FIG._10A

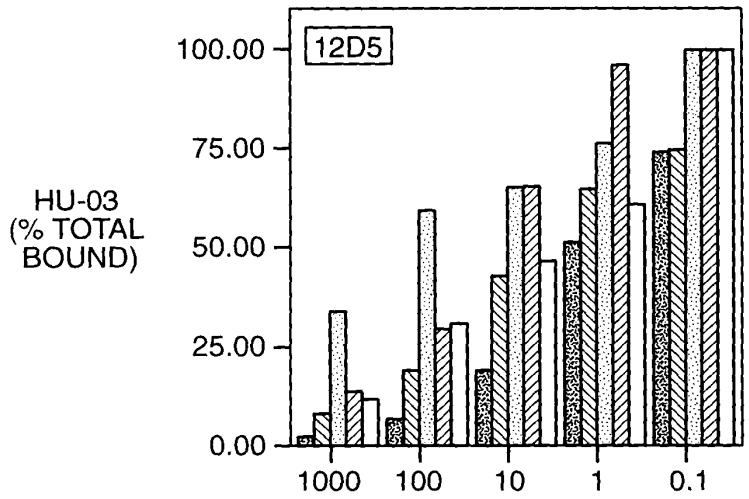

FIG._10B

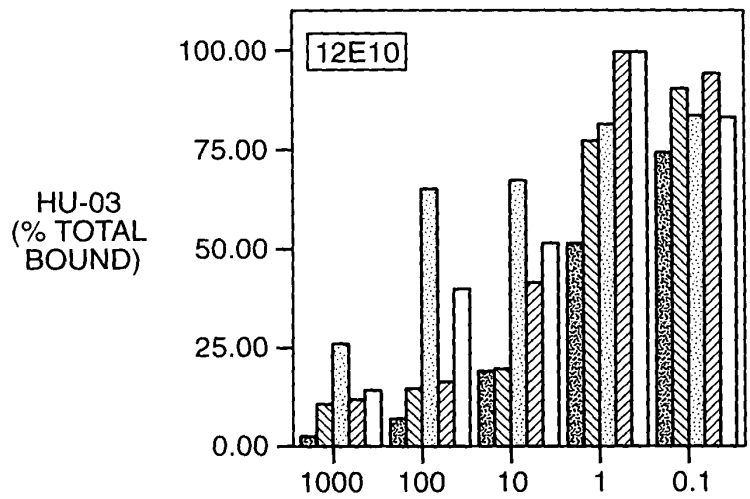

FIG._10C

SUBSTITUTE SHEET (RULE 26)

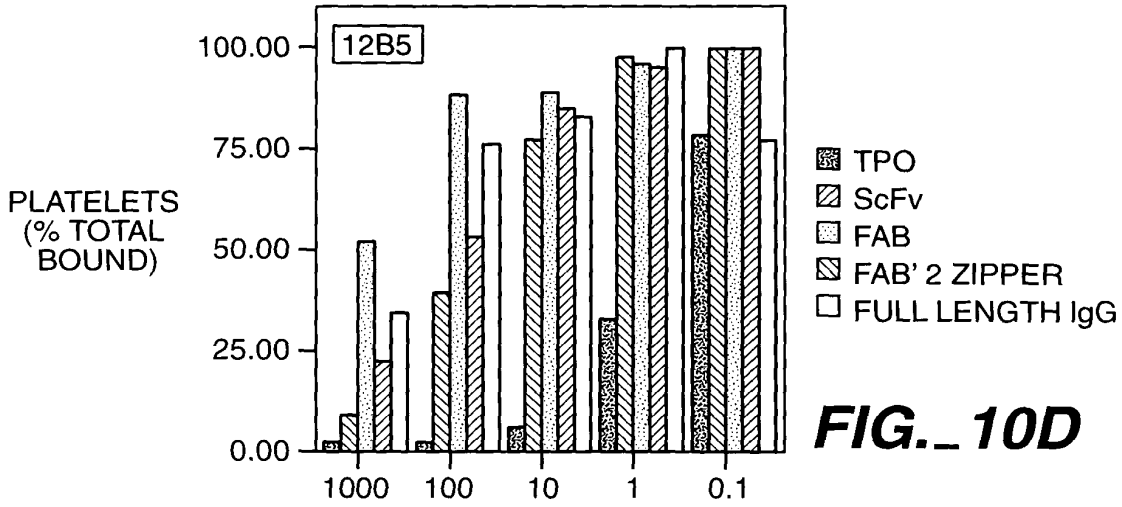

FIG._10D

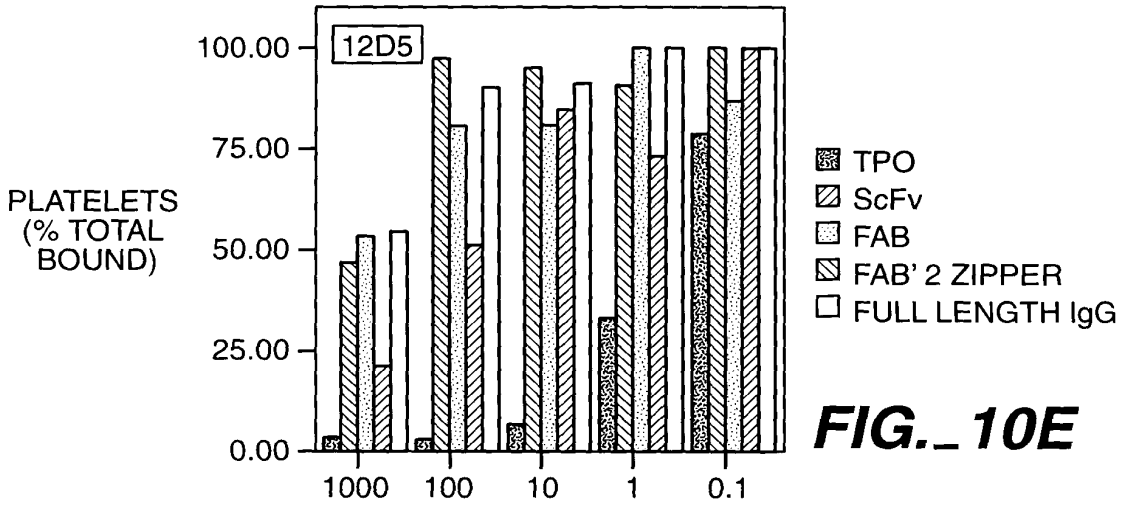

FIG._10E

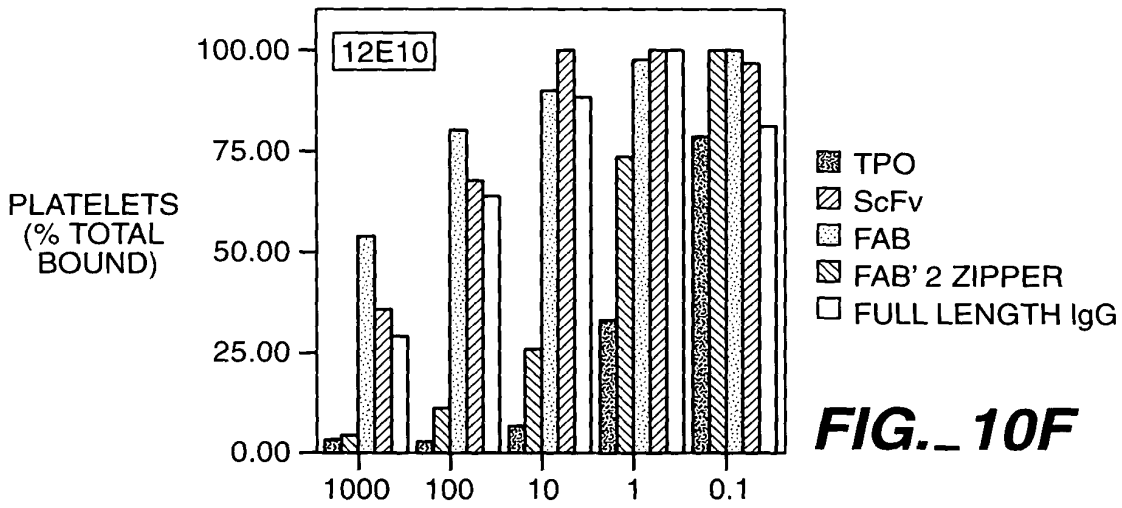

FIG._10F

09/750,464 12/26/00